```
Sequence 13, Appl
Sequence 12, Appl
Sequence 9, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Appli
Sequence 371, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Appli
                                                                         November 17, 2003, 16:26:54; Search time 21 Seconds (without alignments) 163.199 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8, Ar
Sequence 192,
Sequence 332,
Sequence 192,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 332,
Sequence 189,
Sequence 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 14,
Sequence 10,
                                                                                                                                                    1 AVITGACDKDSQCGGGMCCA......LPGLACLRTSFNRFICLAQK 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                328717
                                                                                                                                                                                                                                                                                                                                                                 GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-712-529-2
US-09-996-243-371
US-09-161-241-14
US-09-161-241-11
US-09-161-241-11
US-09-161-241-11
US-09-161-241-13
US-09-161-241-13
US-09-161-241-13
US-09-161-241-13
US-09-161-241-13
US-09-161-241-9
US-09-161-241-9
US-09-188-930-332
US-09-188-930-332
US-09-312-283C-192
US-09-312-283C-192
US-09-312-283C-193
US-09-312-283C-193
US-08-08-489-847-189
US-08-08-532-384-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-895-232-1
US-08-882-046-7
US-09-068-740A-6
US-09-068-740A-7
US-09-199-865-1
US-08-400-159-6
US-08-882-046-2
US-08-882-046-2
                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                       328717 segs, 42310858 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                 OM protein - protein search, using sw model
                                                                                                                                                                                            Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                              US-10-016-481A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2471
                                                                                                                                                                               BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            711
688.55
688.55
688.55
688.55
688.55
688.55
688.55
                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71.5
                                                                                                                              Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90.5
73.5
73.5
73.5
73.5
                                                                                                                                                                                                                                                                                                                                                                  Database :
                                                                                                                                                         Sequence:
                                                                                                                                                                                                                       Searched:
                                                                           Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Result
```

28	68.5	14.9	1218	4	US-09-068-740A-11	Sequence 11, Appl	_
29	68.5	14.9	1219	m	US-08-882-046-5	Sequence 5, Appli	
30	68.5	14.9	3075	7	US-08-460-309-5	Sequence 5, Appli	•н
31	68.5	14.9	3075	7	US-08-125-077-5	Sequence 5, Appli	٠,
32	66.5	14.4	661	н	US-08-399-986B-5	Sequence 5, Appli	٠н
33	66.5	14.4	661	N	US-08-493-754A-5	Seguence 5, Appli	٠,
34	65	14.1	1248	'n	US-08-882-046-6	Sequence 6, Appli	
32	64	13.9	235	4	US-09-620-405B-487	Sequence 487, App	ρ
36	64	13.9	235	4	US-09-604-287A-487	Seguence 487, App	ρ
37	64	13.9	505	4	US-09-620-405B-478	Sequence 478, App	Ω
38	64	13.9	505	4	US-09-620-405B-485	Sequence 485, App	Ω
39	64	13.9	505	4	US-09-604-287A-478	٠	Ω
40	64	13.9	505	4	US-09-604-287A-485	Sequence 485, App	Q,
41	63.5	13.8	2321	4	US-09-230-652-2	Sequence 2, Appli	·H
42	62.5	13.6	1193	N	US-08-400-159-10	Sequence 10, Appl	4
43	62.5	13.6	1193	m	US-08-611-729A-10	Sequence 10, Appl	4
44	62.5	13.6	1940	?	US-08-644-271-30	Sequence 30, Appl	d
45	62.5	13.6	1940	4	US-09-077-955-34	Sequence 34, Appl	d

ALIGNMENTS

```
1 AVITGACDKDSQCGGGMCCAVSIWVKSIRICTPMGKLGDSCHPLTRKVPFFGRRMHHTCP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28 AVITGACDKDSQCGGGMCCAVSIWVKSIRICTPMGKLGDSCHPLTRKVPFFGRRMHHTCP 87
                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 461; DB 4; Length 108; 100.0%; Pred. No. 4e-44; tive 0; Mismatches 0; Indels (
                                                                    GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Bishop, Paul D.
APPLICANT: Bishop, Paul D.
APPLICANT: Thompson, Penny P.
ITLE OF INVENTION: Human Zven Proteins
FILE REPERENCE: 99-81
CURRENT APPLICATION NUMBER: US/09/712,529
CURRENT APPLICATION DOS: 7
                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88 CLPGLACLRTSFNRFICLAQK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 371, Application US/0996243 Patent No. 6478825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 CLPGLACLRISFNRFICLAQK 81
                                // Sequence 2, Application US/09712529
// Patent No. 6485938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ferrara, Napoleone
Fong, Sherman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Bakerazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
                                                                                                                                                                                                                                                                                                                                                                                                                                        81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Desnoyers, Luc
Eaton, Dan L.
                                                                                                                                                                                                                                                                                                                       TYPE: PRT
CRGANISM: Homo sapiens
US-09-712-529-2
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 2
US-09-996-243-371
                                                                                                                                                                                                                                                                                                       108
RESULT 1
US-09-712-529-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT;
APPLICANT;
APPLICANT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                         LENGIH:
                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
```

Godowski, Paul J.

Sequence 6, Sequence 7,

1187

Sequence

Sequence (Sequence (Sequen

Sequence